

FT230" E2E4E660

Human 33410

Carboxylesterase Domain

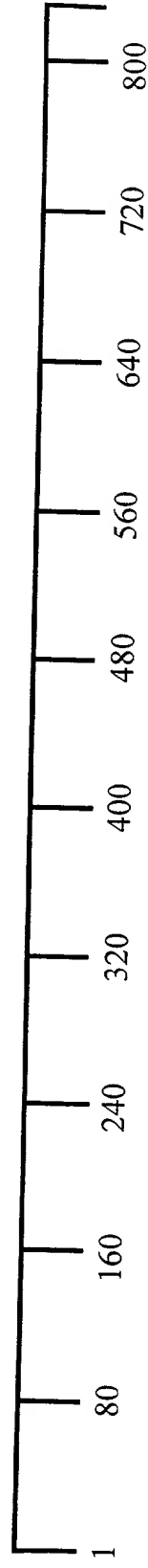
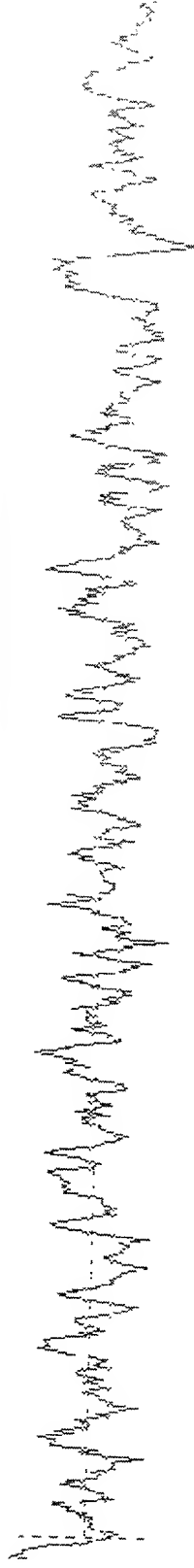


FIG. 1

COesterase: domain 1 of 1, from 42 to 601: score 440.0, E = 2.1e-128	
	*->llVatnnVlcGkvrGvnektnd...geqsvysFlGIPYAEPPVGnLR
Fbh33410FL	42 ++V+t + G vrGv++ ++n+ g +v FlG+PYA PP+G R PVVNTAY---GRVRGVRRELNNeilG--PVVQFLGVPYATPPLGARR 83
Fbh33410FL	84 FkaPqPYkepWsdvldAtkyppsClQdddfgfsldLKva.lkmlslgwn F +P+ + W +v++At+ pp+C+Q+ g +++ +ml+ ++ FQPPEA-PASWPGVRNATTLPPACPQNLH-G-----ALpAIMLPVWFT 124
Fbh33410FL	125 klvg.....lklSEDCLYLNvytPkntkpns..... ++ + +sEDCLYLN y+P + p +++++ + +++++ + DNLEaaatyvQNQSEDCLYLNLYVPTEDGPLTkkrdcatlnppdttdirdp 174
Fbh33410FL	175 .klPvmVwIhGGGFmfGsgshlplslydgeslaregnViVsiNYRLGpl +k Pvm + hGG +m G+g + dg+ la+ gnViV ++NYRLG+l gKKPVMLFLHGGSYMEGTG-----NMFDGSVLAAYGNVIVATLNYRLGVL 219
Fbh33410FL	220 GFLstgddklpgsGNyGLlDQrlALKWVqdNIaaFGGDPnsVTifGeSAG GFLstgd + GNYGLlDQ+ AL+W +NIa+FGGDP+++TifG AG GFLSTGDQAAK--GNyGLLDQlQALRWLSENIaHFGGDPERITIFGSGAG 267
Fbh33410FL	268 aaSVsl1111sngGDNppsskgLFhRAIsqSGsalspwaiquesnargrak a+ V ll+ls +s+gLf++AI qSG+a+s w++ + ++ ASCVNLLILS-----HHSEGLFQKAIAQSGTAISSWSVNYQP--LKYTR 309
Fbh33410FL	310 elarllGCnetssselldCLRsksaeeLleatrsflfeyvpflplflaF la+++GC+++s+e ++CLR+k+++eL++ +++++y + + LLAAKVGCDREDSAEAVECLRRKPSRELVDQDV--QPARYHIAFG----- 352
Fbh33410FL	353 gPvVDGdDapeafipedPeelikeGkfadvPyliGvtkdEGgyfaamlln PvVDGd ++p+dPe+l +G f + ++liGv++ EG+ f + -PVVDGD-----VVPDDPEILMQQGEFLNYDMLIGVNQGEGLKFV----E 392
Fbh33410FL	393 asskgedelkketnpdvwllellkyllfyasealnikdMddladvlekYp +s+ ted ++ ++ + ++ l++ +e + d l +++++ Y+ DSAESEDGVSASAFDF-TVSNFVDNLYGYPEGK-----DVLRETIKFMYT 436
Fbh33410FL	437 gdvdffsvesrkpnlgdmltDl1FkcptrvaadlhakhggsPvYaYvfdh +++d+ e r++ l+ ++tD+ + p +va ++ +++ +sPvY+Y f h DWADRDNGEMRRKTLALFTDhQWVAP-AVATAKLHADYQSPVYFYTFYH 485
Fbh33410FL	486 pasfgigQflakrvdpeffgavHgdEiffvFgnpllkeqlyka...teee + + +pe+ a HgdE+++vFg+p + ++ + + ++ + HCQ-----AEGRPEWADAAGDELPHYVFGVPMVGATDLFFcfnfSKND 527
Fbh33410FL	528 eksssktmmnywanFAktGnPn....ngts.....nglvvWpkytse +++s ++m yw+nFAktG+Pn++ + +t +++++++vW k++s+ VMLS-AVVMTYWTNFAKTGDPNqpvpQDTKfihtkpnrfEEVVWSKFNSK 576
Fbh33410FL	577 eqkYsl1111ttitaqklkardprkvlcnfw<-* e +l+i l+ +++++a++ +fw EKQ-YLHIGLKPRVRDNYRANK-----VAFW 601

Figure 2

CLUSTAL W (1.74) multiple sequence alignment

Fbh33410FL
 ratNL2 = *rat neuromycin 2*
 MWLLALCLVGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVGRVRELN
 MWLLALCLVGLAGAQRGGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVGRVRELN

Fbh33410FL
 ratNL2
 EILGPVVQFLGVPIATPPLGARRFQPPEAPASWPGVRNATTLPPACQNLHGALPAIMLP
 EILGPVVQFLGVPIATPPLGARRFQPPEAPASWPGVRNATTLPPACQNLHGALPAIMLP

Fbh33410FL
 ratNL2
 VWFTDNLEAAATYVQNQSEDCLYLNLYVPTEDGPLTKKRDEATLNPPDIDIRDPGKKPVM
 VWFTDNLEAAATYVQNQSEDCLYLNLYVPTEDGPLTKKRDEATLNPPDIDIRDSGKKPVM

Fbh33410FL
 ratNL2
 LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNRYRLGVLGFLSTGDQAAKAGNYGLLDQIQ
 LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNRYRLGVLGFLSTGDQAAKAGNYGLLDQIQ

Fbh33410FL
 ratNL2
 ALRWLSENIHAFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIASGTAISSWSV
 ALRWLSENIHAFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAIASGTAISSWSV

Fbh33410FL
 ratNL2
 NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKPSRELVDQDVQPARYHIAFGPVVDGDVV
 NYQPLKYTRLLAAKVGCDREDSAEAVECLRRKSSRELVDQDVQPARYHIAFGPVVDGDVV

Fbh33410FL
 ratNL2
 PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
 PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY

Fbh33410FL
 ratNL2
 PEGKDVLRETIKFMYTDWADRDNGEMRRKTLLALFTDHQWVAPAVATAKLHADYQSPVYF
 PEGKDVLRETIKFMYTDWADRDNGEMRRKTLLALFTDHQWVAPAVATAKLHADYQSPVYF

Fbh33410FL
 ratNL2
 YTFYHHCQAEGRPEWADAAHGDELPIYVFGVPMVGATDLFPCNFSKNDVMLS AVVM TYWTN
 YTFYHHCQAEGRPEWADAAHGDELPIYVFGVPMVGATDLFPCNFSKNDVMLS AVVM TYWTN

Fbh33410FL
 ratNL2
 FAKTGDPNQVPVQDTKFIHTKPNRFEEVWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
 FAKTGDPNQVPVQDTKFIHTKPNRFEEVWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF

Fbh33410FL
 ratNL2
 WLELVPHLHNLHTELF TTTTTRLPYATRWP RP P-AGAPGTRRPPPPATLPPEPEPEPGP
 WLELVPHLHNLHTELF TTTTTRLPYATRWP RP TPGPGTSGTRRPPPPATLPPESDIDLGP

Fbh33410FL
 ratNL2
 RAYDRFP GDSRDYSTELSVTVAVGASLLFLN ILAFAALY YKDRRQELRCRRLSPPGGSG
 RAYDRFP GDSRDYSTELSVTVAVGASLLFLN ILAFAALY YKDRRQELRCRRLSPPGGSG

Fbh33410FL
 ratNL2
 SGVPGGGPLLPAAGREL PEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDD
 SGVPGGGPLLPTAGREL PEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDD

Fbh33410FL
 ratNL2
 VPLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPFPPTATSHNNTLPHPHSTTRV
 VPLLAPGALTLLPSGLGPPPPPPPSLHPFGFPFPFPPTATSHNNTLPHPHSTTRV

Figure 3

CLUSTAL W (1.74) multiple sequence alignment

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Fbh33410FL      MWLLALCLVGLAGAQRGGGPGGGAPGGPGLGLGSLGEERFPVVNTAYGRVRGVRRELNN
KIAA1366      -----

Fbh33410FL      EILGPVVQFLGVPYATPPLGARRFQPPEAPASWPGVRNATTLPPACPQNLHGALPAIMLP
KIAA1366      -----

Fbh33410FL      VWFTDNLEAAATYVQNQSEDCLYLNLVPTEDGPLTKKRDEATLNPPDTDIRDPGKKPVM
KIAA1366      -----

Fbh33410FL      LFLHGGSYMEGTGNMFDGSVLAAYGNVIVATLNYRLGVLGFLSTGDQAAKGNYGLLDQIQ
KIAA1366      -----

Fbh33410FL      ALRWLSENI AHFGGDPERITIFGSGAGASCVNLLILSHHSEGLFQKAI AQSGTAISSWSV
KIAA1366      -----KAIAQSGTAISSWSV
                        *****

Fbh33410FL      NYQPLKYTRL LAAKVGCDREDSAEAVECLRRKPSRELVDQDVQPARYHIAFGPVVDGDVV
KIAA1366      NYQPLKYTRL LAAKVGCDREDSAEAVECLRRKPSRELVDQDVQPARYHIAFGPVVDGDVV
                        *****

Fbh33410FL      PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
KIAA1366      PDDPEILMQQGEFLNYDMLIGVNQGEGLKFVEDSAESEDGVSASAFDFTVSNFVDNLYGY
                        *****

Fbh33410FL      PEGKDVLR ETIKFMYTDWADRDNGEMRRKTL LALFTDHQWVAPAVATAKLHADYQSPVYF
KIAA1366      PEGKDVLR ETIKFMYTDWADRDNGEMRRKTL LALFTDHQWVAPAVATAKLHADYQSPVYF
                        *****

Fbh33410FL      YTFYHHCQAEGRPEWADAAHGDEL PYVFGVPMVGATDLFPCNFSKNDVMLS AVVM TYWTN
KIAA1366      YTFYHHCQAEGRPEWADAAHGDEL PYVFGVPMVGATDLFPCNFSKNDVMLS AVVM TYWTN
                        *****

Fbh33410FL      FAKTGDPNQPV PQDTKFIHTKPNRFEEVWWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
KIAA1366      FAKTGDPNQPV PQDTKFIHTKPNRFEEVWWSKFNSKEKQYLHIGLKPRVRDNYRANKVAF
                        *****

Fbh33410FL      WLELVPHLHNLHTELF TTTTTRLPPYATRWPPRPPAGAPGTRRPPPPATLPPEPEPEPGPR
KIAA1366      WLELVPHLHNLHTELF TTTTTRLPPYATRWPPRPPAGAPGTRRPPPPATLPPEPEPEPGPR
                        *****

Fbh33410FL      AYDRFPGDSRDYSTELSVTVAVGASLLFLN ILAFAALYYKRDRRQELRCRRLSPPGGSGS
KIAA1366      AYDRFPGDSRDYSTELSVTVAVGASLLFLN ILAFAALYYKRDRRQELRCRRLSPPGGSGS
                        *****

Fbh33410FL      GVPGGGPLLPAA GRELPPEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDDV
KIAA1366      GVPGGGPLLPAA GRELPPEEELVSLQLKRGGGVGADPAEALRPACPPDYTLALRRAPDDV
                        *****

Fbh33410FL      PLLAPGALTLLPSGLGPPPPPPPPSLHPFGFPFPPPPPTATSHNNTLPHPHSTTRV
KIAA1366      PLLAPGALTLLPSGLGPPPPPPPPSLHPFGFPFPPPPPTATSHNNTLPHPHSTTRV
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Figure 4